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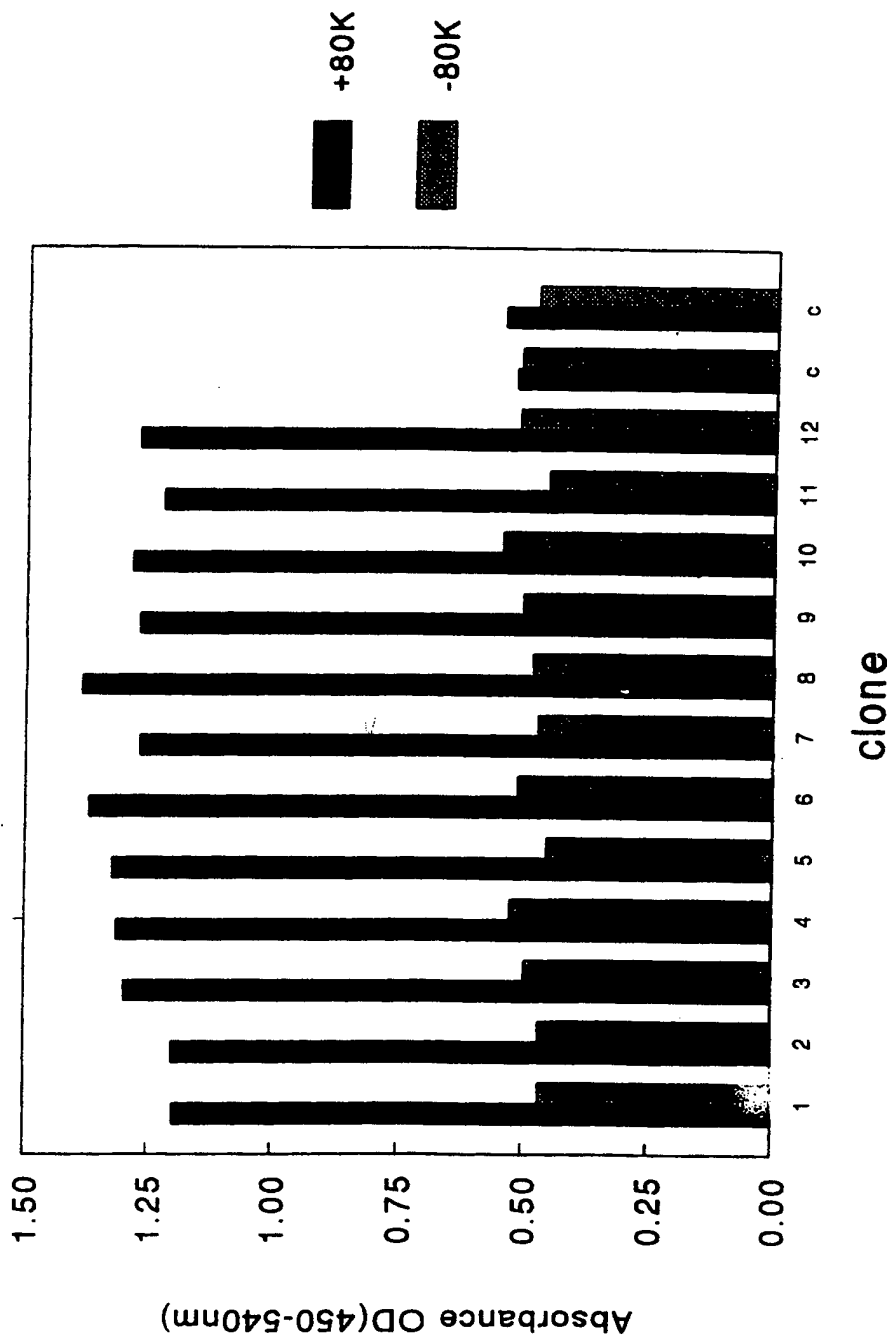


Figure 1

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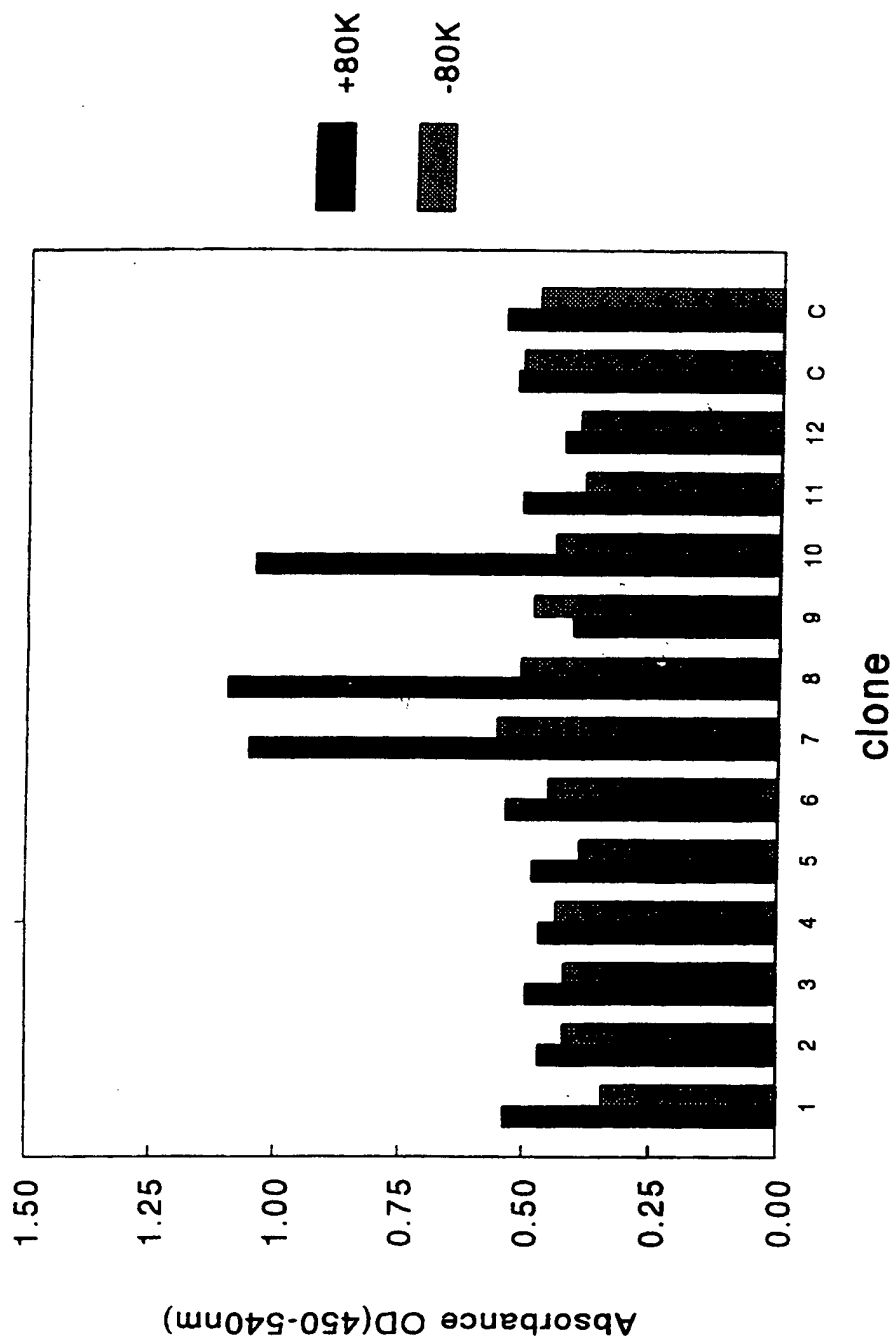


Figure 2

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[illegible][illegible]

CDR3													FRAMEWORK 4																		
95	96	97	98	99	100	a	b	c	d	e	f	g	h	i	j	k	l	m	101	102	103	104	105	106	107	108	109	110	111	112	113
CAA	CAG	AAC	GGC	TGG	TAC	GAA	GGA	CCG	TTG	CTT	GAG	CCG	AGG	CCT	GAT	GCT	CTT	GAT	ATC	TGG	GAG	CAA	GCG	ACA	ATG	GTC	ACC	GTG	TGG	AGT	

[illegible][illegible]

CDR3																FRAMEWORK 4																	
95	96	97	98	99	100	a	b	c	d	e	f	g	h	i	j	k	l	m	n	o	101	102	103	104	105	106	107	108	109	110	111	112	113
CAT	GGG	GGG	GGG	GCT	GCC	TAT	GAA	GAT	GTT	TGG	AGT	GGT	GAG	TAC	CCC	GAA	TAC	TAC	GCT	ATG	GAC	GTC	TGG	GGC	CAA	GGG	ACC	ACG	GTC	ACC	GTG	TGG	AGT

### Figure 3

**Figure 4A**

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Figure 4B

FIG. 4B is a schematic diagram of a system for processing a signal. The system includes a signal source, a signal processor, and a signal output. The signal source provides a signal to the signal processor, which then outputs the signal to the signal output. The signal processor is configured to process the signal in a specific manner, such as filtering or amplification. The signal output is then used for further processing or display.

FR1	CDR1	FR2	CDR2	FR3	CDR3	FR4
1	2	3	4	5	6	7
123456789012345678901234567890	1ab2345	67890123456789	012abc3456789012345	67890123456789012abc345678901234	567890abcde fghijklmno12	34567890123
QVOLVQSGAEVKKPGASVKVSKASGYTFT	S--YGIS	WVRQAPGQGLEMMG	WISA--YNGNTNYAKLOG	RVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR	DGGGGAYEDVMSGEYPEYYAMDV	WGQGTTVTVSS
--L-AT--	--D--	--V--	--I--S--D--F--	--RR--		
--L-AT--	--D--		--I--S--D--F--	--RR--		
--L-A--R--						

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CDR3

EL-14	QQNGGWYEGPLLEPRPD--ALDI
	.  .
IT-2	DGGGAYEDVWSGEYPEYYAMDV

Figure 4C

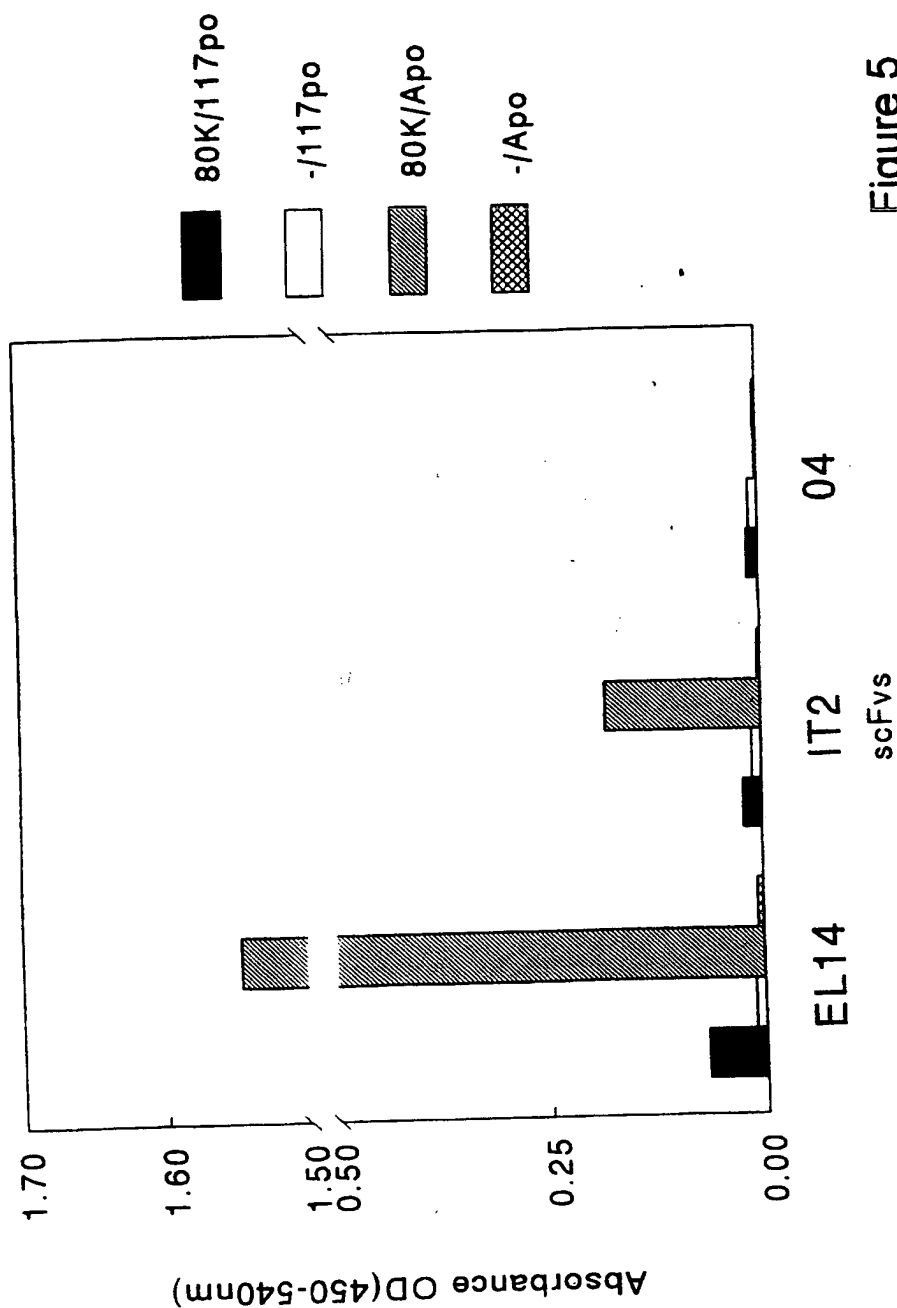


Figure 5

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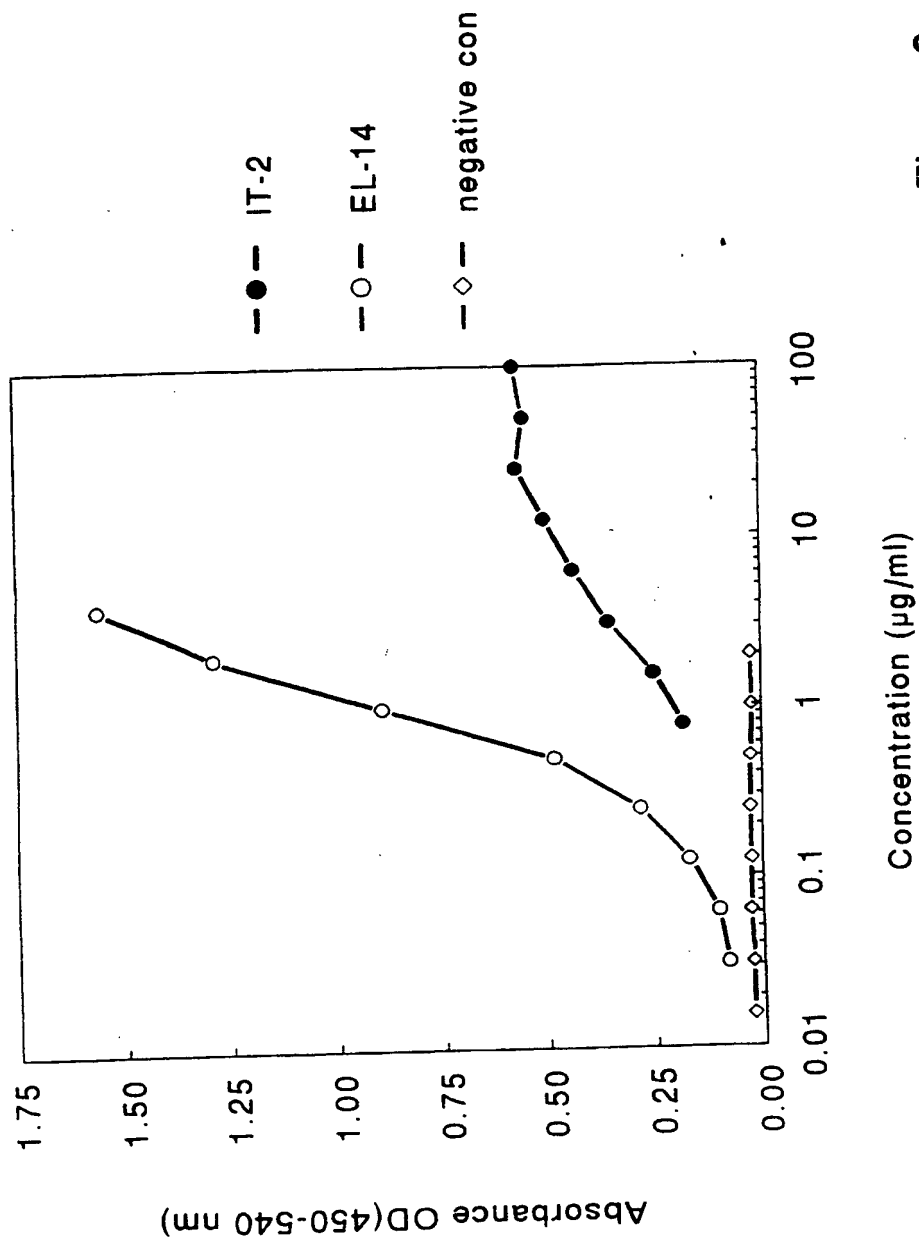


Figure 6



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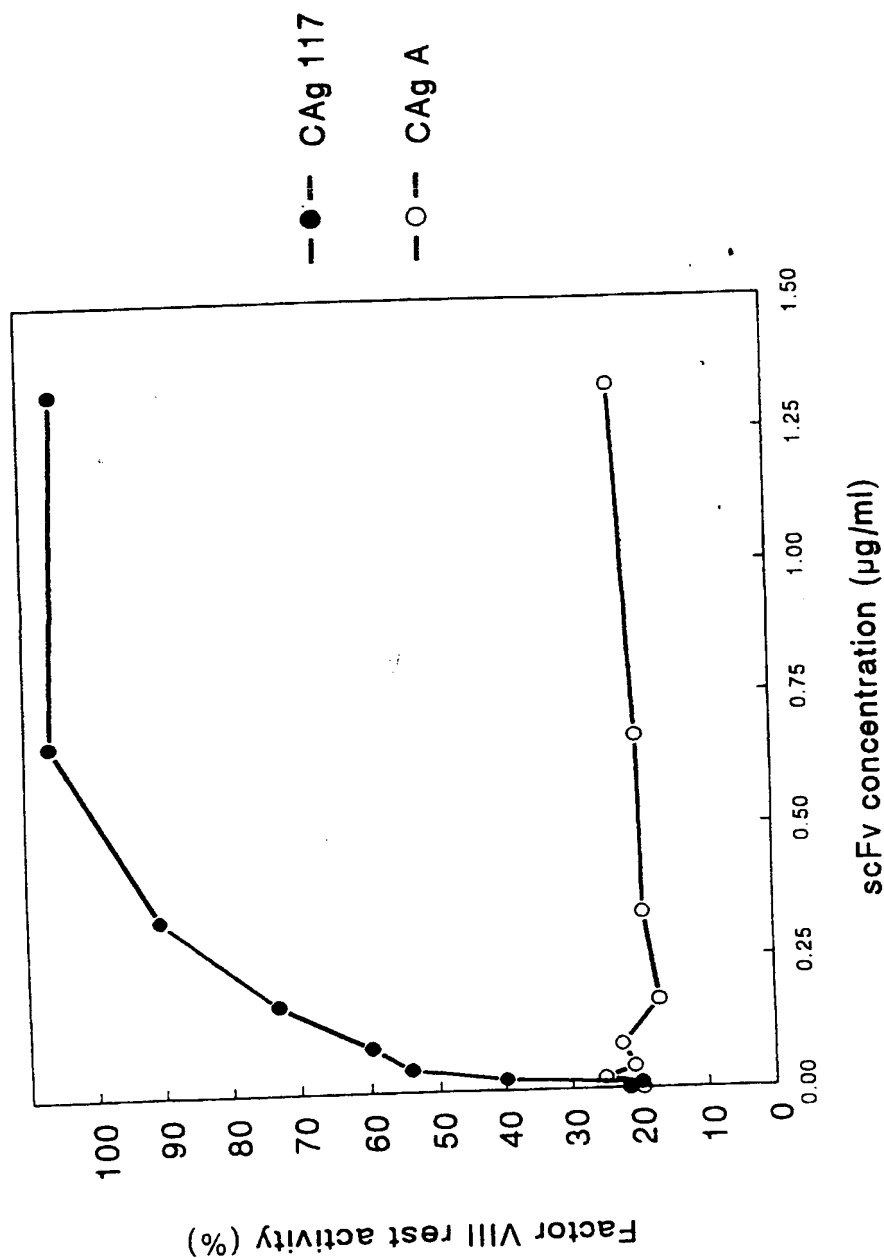


Figure 7A NEUTRALIZATION BY scFv EL-14

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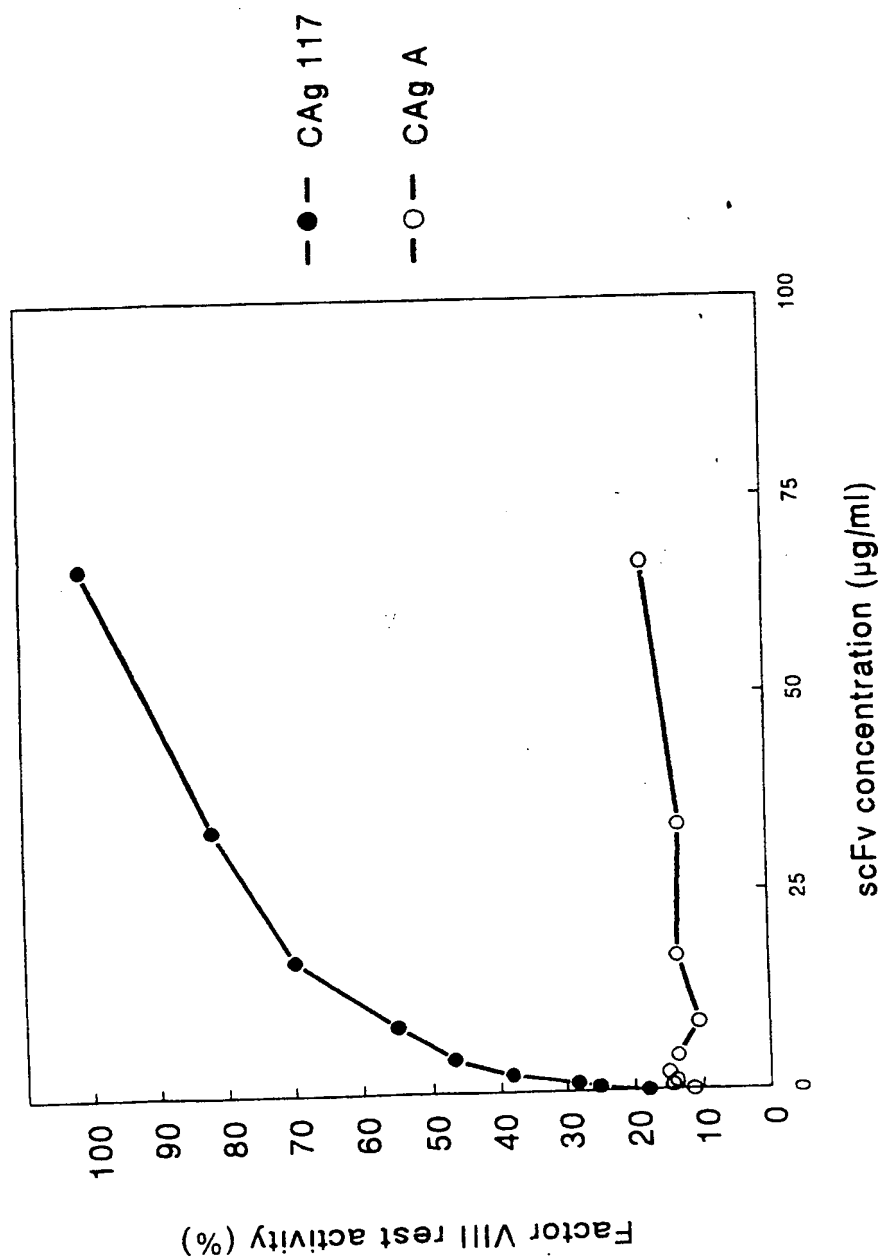
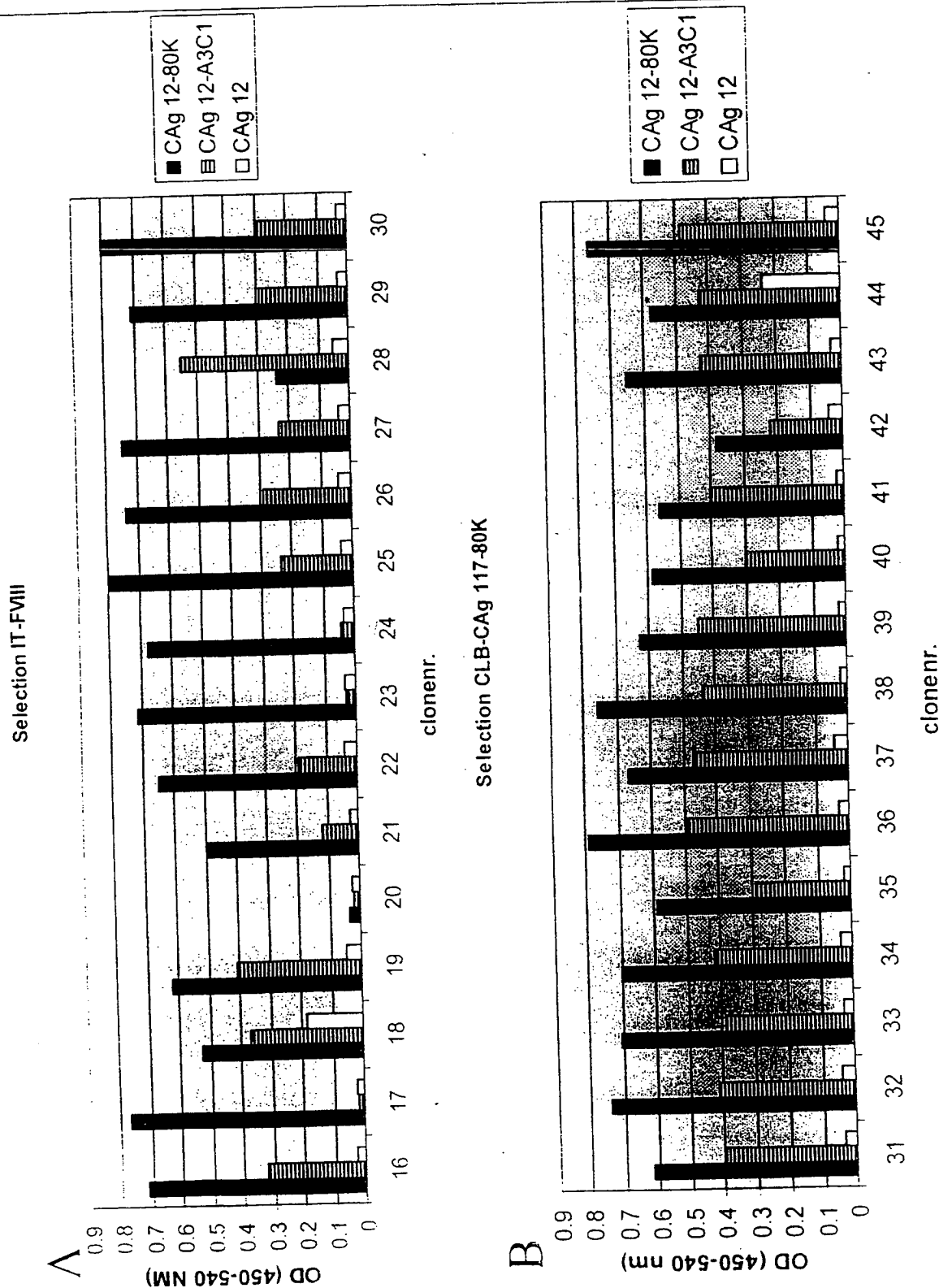


Figure 7B NEUTRALIZATION BY scFv IT-2

Figure 8



**Figure 9A**

[illegible]

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+1 Gln Val Gln Leu Leu Gln Ser Ala Ala Asp Val Lys Lys Pro Gly Ala Ser  
 CAGGTGCAGC TGTTGCAGTC TGCAGCTGAC GTGAAGAAGC CTGGGGCCTC 50  
 GTCCACGTCG ACAACGTCAG ACGTCGACTG CACTTCTTCG GACCCCGGAG

+1 Val Lys Val Ser Cys Thr Ala Ser Gly Tyr Ile Phe Thr Ser Tyr Asp Ile  
 AGTGAAGGTC TCCTGTACGG CTTCTGGATA CATCTTCACC AGTTATGATA 100  
 TCACTTCCAG AGGACATGCC GAAGACCTAT GTAGAAGTGG TCAATACTAT

+1 Asn Trp Val Arg Gln Ala Thr Gly Gln Gly Leu Glu Trp Met Gly Trp  
 TCAACTGGGT GCGACAGGCC ACTGGACAAG GGCTTGAGTG GATGGGATGG 150  
 AGTTGACCCA CGCTGTCCGG TGACCTGTTC CCGAACTCAC CTACCCTACC

+1 Met Asn Pro Asn Ser Gly Asn Ala Gly Phe Ala Gln Lys Phe Lys Gly Arg  
 ATGAATCCTA ACAGTGGTAA CGCAGGCTTT GCACAGAAGT TTAAGGGCAG 200  
 TACTTAGGAT TGTCACCATT GCGTCCGAAA CGTGTCTTCA AATTCCTCGTC

+1 Leu Thr Leu Thr Arg Asp Thr Ser Thr Ser Thr Ala Tyr Met Glu Leu Arg  
 ACTCACCTTG ACCAGGGACA CTTCCACAAG CACAGCCTAC ATGGAGCTGA 250  
 TGAGTGGAAC TGGTCCCTGT GAAGGTGTTC GTGTCGGATG TACCTCGACT

+1 Arg Leu Glu Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Cys Asp  
 GGAGACTGGA ATCTGAGGAC ACGGCCGTGT ATTACTGTGC GAGATGTGAC 300  
 CCTCTGACCT TAGACTCCTG TGCCGGCACA TAATGACACG CTCTACACTG

+1 Thr Thr Leu Leu Ile Trp Phe Gly Pro Ala Pro Tyr Tyr Asp Ser Trp Gly  
 ACCCACTCT TAATCTGGTT CGGGCCCGCC CCCTACTATG ACTCCTGGGG 350  
 TGGTGTGAGA ATTAGACCAA GCCCGGGCGG GGGATGATAC TGAGGACCCC

+1 Gln Gly Thr Leu Val  
 CCAGGGAAC CTAGTC  
 GGTCCCTTGA GATCAG 400

Figure 9B

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+1 Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Lys Ser-  
 CAGGTGCAAC TGGTGCAGTC TGGGGGAGGC TTGGTACAGC CTGGCAAGTC 50  
 GTCCACGTTG ACCACGTCAG ACCCCCTCCG AACCATGTCG GACCGTTCAG  
 -1 Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Asp Tyr Ala Ile-  
 CCTGAGACTC TCCTGTGCAG CCTCTGGATT CACATTTGGC GATTATGCCA 100  
 GGACTCTGAG AGGACACGTC GGAGACCTAA GTGTAAACCG CTAATACGGT  
 +1 His Trp Val Arg Gln Ala Pro Gly Glu Gly Leu Glu Trp Val Ser Gly  
 TACACTGGGT CCGGCAAGCT CCAGGGGAGG GCCTGGAGTG GGTCTCAGGT 150  
 ATGTGACCCA GGCCGTTCTGA GGTCCCCTCC CGGACCTCAC CCAGAGTCCA  
 -1 Val Thr Trp Ser Gly Thr Thr Ile Gly Phe Ala Asp Ser Val Lys Gly Arg-  
 GTTACTTGGA GTGGTACTAC TATAGGCTTT GCGGACTCTG TGAAGGGCCG 200  
 CAATGAACCT CACCATGATG ATATCCGAAA CGCCTGAGAC ACTTCCCGGC  
 +1 Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Tyr Met Asn  
 ATTCACCATC TCCAGAGACA ACGCCAAGAA TTCCCTGTAT CTGTACATGA 250  
 TAAGTGGTAG AGGTCTCTGT TCGGGTTCTT AAGGGACATA GACATGTACT  
 +1 Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys Ala Leu Pro Tyr  
 ACAGTCTGAG AGCTGAAGAC ACGGCCTTGT ATTATTGTGC CTTACCATAT 300  
 TGTCAGACTC TCGACTTCTG TGCCGGAACA TAATAACACG GAATGGTATA  
 -1 Ile Asn Ser Ser Asn Tyr Arg Arg Gly Val Ala Ala Phe Asp Ile Trp Gly-  
 ATCAACTCGT CCAACTACAG AAGAGGGGTC GCTGCCTTCG ATATCTGGGG 350  
 TAGTTGAGCA GGTTGATGTC TTCTCCCCAG CGACGGAAGC TATAGACCCC  
 +1 Gln Gly Thr Met Val Thr Val Ser Ser  
 CCAAGGGACA ATGGTCACCG TGTCGAGT 400  
 GGTTCCTGT TACCAGTGGC ACAGCTCA

Figure 9C

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+1 -Glu- Val- Gln- Leu- Val- Glu- Ser- Gly- Gly- Gly- Leu- Val- Gln- Pro- Gly- Arg- Ser-  
 GAGGTGCAGC TGGTGGAGTC TGGGGGAGGC TTGGTACAGC CTGGGAGGTC 50  
 CTCCACGTCG ACCACCTCAG ACCCCCTCCG AACCATGTCG GACCCTCCAG  
 +1 -Leu- Arg- Leu- Ser- Cys- Val- Asp- Ser- Gly- Leu- Thr- Phe- Ser- Ser- Tyr- Gly- Met  
 CCTGAGACTC TCCTGTGTAG ACTCTGGACT CACCTTCAGT AGTTATGGCA 100  
 GGACTCTGAG AGGACACATC TGAGACCTGA GTGGAAGTCA TCAATACCGT  
 +1 -His- Trp- Val- Arg- Gln- Ala- Pro- Gly- Ala- Gly- Leu- Glu- Trp- Val- Ala- Val-  
 TGCACCTGGGT CCGCCAGGCT CCAGGCGCGG GGCTGGAGTG GGTGGCCGTT 150  
 ACGTGACCCA GCGGGTCCGA GGTCCGCGCC CCGACCTCAC CCACCGGCAA  
 -1 -Ile- Ser- Tyr- Asp- Gly- Asn- Asp- Lys- Tyr- Tyr- Ala- Asp- Ser- Val- Lys- Gly- Arg-  
 ATTCATACG ACGGAAATGA TAAATATTAT GCAGACTCCG TGAAGGGCCG 200  
 TAAAGTATGC TGCCTTTACT ATTTATAATA CGTCTGAGGC ACTTCCCGGC  
 +1 -Phe- Ala- Ile- Ser- Arg- Asp- Asn- Ala- Lys- Asn- Thr- Leu- Tyr- Leu- Gln- Met- Asn  
 ATTCGCCATC TCCAGAGACA ATGCCAAGAA CACGCTGTAT CTGCAAATGA 250  
 TAAGCGGTAG AGGTCTCTGT TACGGTTCTT GTGCGACATA GACGTTTACT  
 +1 -Ser- Leu- Thr- Ile- Glu- Asp- Thr- Ala- Val- Tyr- Tyr- Cys- Ala- Lys- Asp- Leu-  
 ACAGCCTGAC AATAGAGGAC ACGGCTGTCT ATTATTGTGC GAAAGATCTC 300  
 TGTCGGACTG TTATCTCCTG TGCCGACAGA TAATAACACG CTTTCTAGAG  
 +1 -Ile- Glu- Ser- Asn- Ile- Ala- Glu- Ala- Leu- Trp- Gly- Gln- Gly- Thr- Leu- Val- Thr-  
 ATAGAATCAA ATATTGCGGA GGCCCTCTGG GGCCAGGGAA CCCTGGTCAC 350  
 TATCTTAGTT TATAACGCCT CCGGGAGACC CCGGTCCCTT GGGACCAGTG  
 +1 -Val- Ser- Ser-  
 CGTGTCGAGT  
 GCACAGCTCA 400

Figure 9D

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+1 Glu Val Gln Leu Val Lys Ser Gly Glu Gly Leu Val Lys Pro Gly Gly Ser-  
 GAGGTGCAGC TGGTGAAGTC TGGGGAAGGC CTGGTCAAGC CTGGGGGGTC 50  
 CTCCACGTCG ACCACTTCAG ACCCCTTCCG GACCAGTTCG GACCCCCCAG  
 -1 Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Arg Tyr Asp Ile-  
 CCTGAGACTC TCCTGTGCAG CCTCTGGATT CACCTTCAGG AGATATGATA 100  
 GGA CTCTGAG AGGACACGTC GGAGACCTAA GTGGAAGTCC TCTATACTAT  
 +1 His Trp Val Arg Gln Thr Pro Gly Lys Gly Leu Glu Trp Val Ser Ser-  
 TCCACTGGGT CCGCCAGACT CCAGGGAAGG GCCTGGAGTG GGTCTCATCC 150  
 AGGTGACCCA GGCGGTCTGA GGTCCCTTCC CGGACCTCAC CCAGAGTAGG  
 +1 Ile Ser Ser Gly Gly Asn Tyr Ile Asp Tyr Ala Asp Ser Val Lys Gly Arg-  
 ATCAGTAGTG GTGGTAATTA CATAGACTAC GCAGACTCTG TGAAGGGCCG 200  
 TAGTCATCAC CACCATTAAT GTATCTGATG CGTCTGAGAC ACTTCCCGGC  
 +1 Phe Thr Ile Ser Arg Asp Asn Ala Asn Asn Val Val Tyr Leu Gln Met Asn  
 ATTCAACATC TCCAGAGACA ACGCCAACAA TGTTGTCTAT CTACAAATGA 250  
 TAAGTGGTAG AGGTCTCTGT TGC GGTTGTT ACAACAGATA GATGTTTACT  
 +1 Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Phe Cys Ala Arg Asp Gly  
 ACAGCCTGAG AGCCGAGGAC ATGGCTGTCT ATTTCTGTGC GAGAGATGGG 300  
 TGTCGGACTC TCGGCTCCTG TACCGACAGA TAAAGACACG CTCTCTACCC  
 -1 Thr Ile Phe Gly Ser Ala Ala Thr Trp Arg Ala Phe Asp Ile Trp Gly Arg-  
 ACGATTTTTG GATCGGCGGC GACCTGGCGG GCTTTTGATA TCTGGGGCCG 350  
 TGCTAAAAAC CTAGCCGCCG CTGGACCGCC CGAAACTAT AGACCCCGGC  
 +1 Gly Thr Met Val Thr Val Ser Ser-  
 GGGGACAATG GTCACCGTGT CGAGT 400  
 CCCCTGTTAC CAGTGGCACA GCTCA

Figure 9E



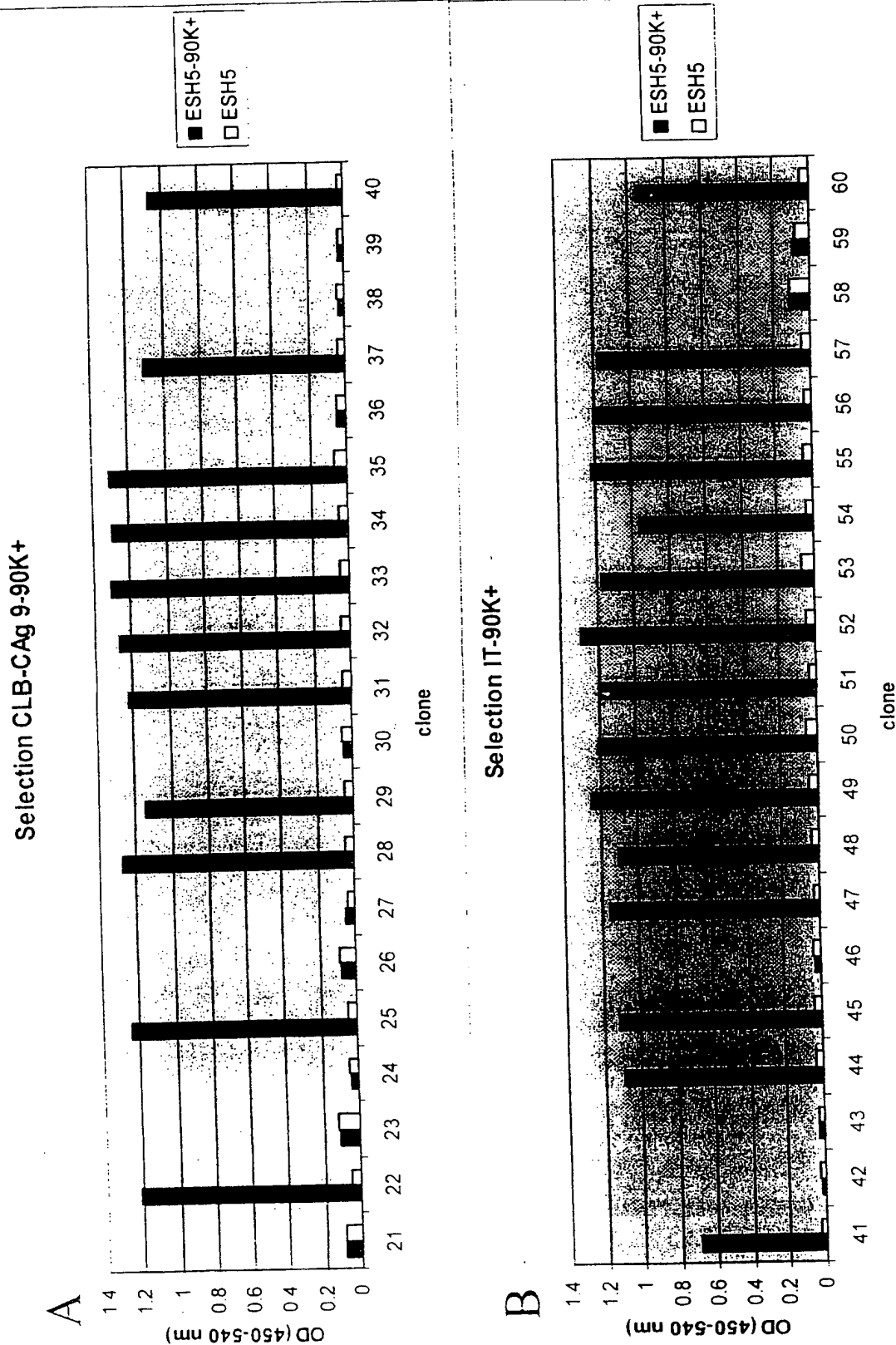


Figure 10

**Deduced protein sequences of isolated FVIII A2 specific scFv**

[illegible]

## Figure 11A

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+1 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser  
 CAGGTGCAGC TGGTGCAGTC TGGGGCTGAG GTGAAGAAGC CTGGGTCCTC 50  
 GTCCACGTCG ACCACGTCAG ACCCCGACTC CACTTCTTCG GACCCAGGAG

+1 Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser His Ala Ile  
 GGTGAAGGTC TCCTGCAAGG CTTCTGGAGG CACCTTCAGC AGTCATGCTA 100  
 CCACTTCCAG AGGACGTTCC GAAGACCTCC GTGGAACTCG TCAGTACGAT

+1 Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Asp  
 TCAGCTGGGT GCGACAGGCC CCTGGACAAG GGCTTGAGTG GATGGGAGAC 150  
 AGTCGACCCA CGCTGTCCGG GGACCTGTTC CCGAACTCAC CTACCCTCTG

+1 Ile Ile Pro Ile Leu Gly Thr Gly Asn Tyr Ala Gln Lys Phe Gln Gly Arg  
 ATCATCCCTA TCCTTGGTAC AGGAACTAC GCACAGAAGT TCCAGGGCAG 200  
 TAGTAGGGAT AGGAACCATG TCCTTTGATG CGTGTCTTCA AGGTCCCGTC

+1 Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser  
 AGTCACGATT ACCGCGGACG AGTCCACGAG CACAGCCTAC ATGGAGCTGA 250  
 TCAGTGCTAA TGGCGCCTGC TCAGGTGCTC GTGTCGGATG TACCTCGACT

+1 Thr Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Glu Leu Asp Trp  
 GCACCCTGAC ATCTGAGGAC ACGGCCGTGT ATTACTGTGA ACTTGACTGG 300  
 CGTGGGACTG TAGACTCCTG TGCCGGCACA TAATGACACT TGAAGTACC

+1 Phe Tyr Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser  
 TTCTATATCT GGGGCCAAGG GACAATGGTC ACCGTGTCGA GT 350  
 AAGATATAGA CCCCAGTTCC CTGTTACCAG TGGCACAGCT CA

Figure 11B

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+1 [Glu] [Val] [Gln] [Leu] [Val] [Glu] [Ser] [Gly] [Gly] [Asp] [Leu] [Val] [Gln] [Pro] [Gly] [Gly] [Ser]  
GAGGTGCAGC TGGTGGAGTC TGGGGGAGAC TTGGTACAGC CTGGGGGGGTC 50  
CTCCACGTCG ACCACCTCAG ACCCCCTCTG AACCATGTCG GACCCCCCAG

+1 [Leu] [Arg] [Leu] [Ser] [Cys] [Ala] [Ala] [Ser] [Gly] [Phe] [Thr] [Phe] [Ser] [Asn] [Phe] [Ala] [Met]  
CCTGAGACTC TCCTGTGCAG CCTCTGGATT CACCTTTAGC AACTTTGCCA 100  
GGACTCTGAG AGGACACGTC GGAGACCTAA GTGGAAATCG TTGAAACGGT

+1 [Ser] [Trp] [Val] [Arg] [Gln] [Ala] [Pro] [Gly] [Lys] [Gly] [Leu] [Glu] [Trp] [Val] [Ala] [Ala]  
TGAGCTGGGT CCGCCAGGCT CCCGGGAAGG GGCTGGAGTG GGTCGCGGCT 150  
ACTCGACCCA GGCGGTCCGA GGGCCCTTCC CCGACCTCAC CCAGCGCCGA

+1 [Ile] [Gly] [Gly] [Arg] [Ser] [Gly] [Thr] [Thr] [Phe] [Tyr] [Ala] [Asp] [Ser] [Val] [Lys] [Gly] [Arg]  
ATTGGCGGTA GAAGTGGTAC CACATTCTAC GCGGACTCCG TGAAGGGCCG 200  
TAACCGCCAT CTTACCATG GTGTAAGATG CGCCTGAGGC ACTTCCCGG

+1 [Phe] [Thr] [Ile] [Ser] [Arg] [Asp] [Asn] [Ser] [Lys] [Asn] [Thr] [Val] [Tyr] [Leu] [Glu] [Met] [Asn]  
GTTCAACATC TCCAGAGACA ATTCCAAGAA CACGGTCTAT CTGGAAATGA 250  
CAAGTGGTAG AGGTCTCTGT TAAGGTTCTT GTGCCAGATA GACCTTTACT

+1 [Ser] [Leu] [Arg] [Ala] [Glu] [Asp] [Thr] [Ala] [Ile] [Tyr] [Tyr] [Cys] [Ala] [Lys] [Arg] [Gly]  
ACAGTCTGAG AGCCGAGGAC ACAGCCATTT ATTACTGTGC GAAAAGAGGG 300  
TGTCAGACTC TCGGCTCCTG TGTCGGTAAA TAATGACACG CTTTCTCTCC

+1 [Arg] [Gly] [Gly] [Tyr] [Lys] [Tyr] [Tyr] [Gly] [Met] [Asp] [Val] [Trp] [Gly] [Gln] [Gly] [Thr] [Thr]  
CGCGGGGGGT ATAAGTATTA TGGGATGGAC GTCTGGGGCC AGGGGACCAC 350  
GCGCCCCCA TATTCATAAT ACCCTACCTG CAGACCCCGG TCCCCTGGTG

+1 [Val] [Thr] [Val] [Ser] [Ser]  
GGTCACCGTG TCGAGT 400  
CCAGTGGCAC AGCTCA

Figure 11C